

CS194 Expression Array Data

Description of Procedure:

Using CN as an example, equivalent amounts of total RNA from 20 different colon normal samples were combined and mRNA was purified from the pool. This mRNA pool represents the sample CN. The normal and tumor tissues used for expression array analysis are listed in Table 1. The mRNA from the tumor and normal tissues were sent to Incyte Genomics where the cDNA was synthesized from the mRNA. The cDNA from both the normal and tumor samples, were labeled with fluorescent dyes Cy3 or Cy5, mixed together and hybridized to human GEM 1-4 cDNA microarray chips (Incyte Genomics). The results are reported as the fold difference expression of CS194 (Incyte microarray clone ID# 1628788) hybridized with normal and tumor sample pools (Fig. 1).

OVARY

OT1 10 TUMOR SAMPLES
OT2 10 TUMOR SAMPLES
ON 20 NORMAL SAMPLES

LUNG

LT7 7 TUMOR SAMPLES
LN7 7 MATCHED NORMAL SAMPLES
LT10 10 TUMOR SAMPLES
LN10 10 NORMAL SAMPLES

BREAST

BT1 10 TUMOR SAMPLES
BT2 10 TUMOR SAMPLES
BN 20 NORMAL SAMPLES

COLON

CT1 10 TUMOR SAMPLES
CT2 10 TUMOR SAMPLES
CN 20 NORMAL SAMPLES

KIDNEY

KT18 18 TUMOR SAMPLES
KN18 18 MATCHED NORMAL SAMPLES
KT5 5 TUMOR SAMPLES
KN5 5 MATCHED NORMAL SAMPLES

Table 1. Normal and tumor tissues used for gene

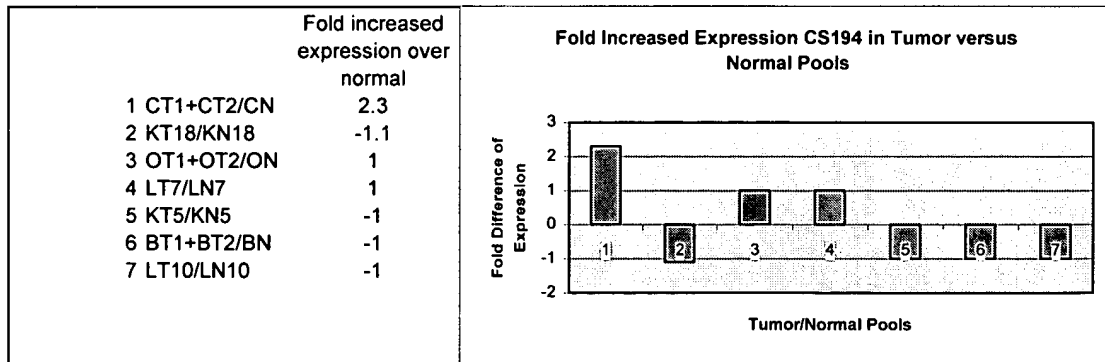


Fig. 1 Fold Increased Expression CS194 in Tumor versus Normal Pools

Summary of Results:

CS194 expression is 2.3 fold higher in the colon tumor tissue pool compared to the colon normal tissue pool (fig. 1).